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 AN12m ATGACGCTATGGGGCTGTGTCTTCCGTAAGGCTTCCCTGGGGGGGGTGGGGGGGGGGTCTCTCCAGCTGGGGTGGC 80
 AN13m ATGACGCTATGGGGCTGTGTCTTCCGTAAGGCTTCCCTGGGGGGGGTGGGGGGGGGGTCTCTCCAGCTGGGGTGGC 80

AN11m CCCCCATCCAGGGGTCAATCTGCTGCTGCTGGCTTCCAGCATGCCAGCAATCTCATCTGTGCTTCAAGCGTACAAAGGCA 16
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 AN13m TCCCATCCAGGGGGTCAAGCTGCTGCTGCTGGCTTCCAGCATGCCAGCAAGCGTACCTCTCCAGCAATCAAGGCA 16

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 AN12m TTTATGACTGCTGGTGGTCCGTAATCCCAAGGCTTCCCTGGGGGGGGTGGGGTAACTGGCCAACTGTATCCG 24
 AN13m TCGTGGCTCTGCTTGTGCTGGCTTCCCAAGGCTTCCCTGGGGGGGGTGGGGTAACTGGCCAACTGTATCCG 24

AN11m TACTTCCCCCCTCCCAAGCTCTCAACTTCCGCTTCAAGGCTAAGTACAAGCGTCTCTCTTGGGGGGTGGGGTGGGGTAA 32
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 AN13m TACTTCCCCCCTCCCAAGCTCTCAACTTCCGCTTCAAGGCTAAGTACAAGCGTCTCTCTTGGGGGGTGGGGTGGGGTAA 32

AN11m GCGCTTCTGGGGCTTCACTTCCCTGGTAACTGGGGTCCGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 40
 AN12m GCGCTTCTGGGGCTTCACTTCCCTGGTAACTGGGGTCCGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 40
 AN13m GCGCTTCTGGGGCTTCACTTCCCTGGTAACTGGGGTCCGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 40

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 AN13m TGGCTTTTGGCTTCACTTCCCTGGTAACTGGGGTCCGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 48

AN11m CTCTCTCAAGATCTCAAGTCTCTTGGGGCTTCCAGGGCTTCAAGGGCTTCAAGGGCTTCAAGGGCTTCAAGGGCTTCA 55
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 AN13m CTCTCTCAAGATCTCAAGTCTCTTGGGGCTTCCAGGGCTTCAAGGGCTTCAAGGGCTTCAAGGGCTTCAAGGGCTTCA 56

AN11m TGGCTTTTGGCTTCACTTCCCTGGTAACTGGGGTCCGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 63
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 AN13m CCGTGGGGGGCTTCCCTGGTAACTGGGGTCCGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 64

AN11m GGAATGATGGGGCTTCAAGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTT 71
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AN11m CAGTCCGGGGGGTAAAGGGGGGGTAAAGGGTAAAGGGTAAAGGGTAAAGGGTAAAGGGTAAAGGGTAAAGGGTAAAGGG 79
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AN11m CAAGGGCTTCTTCAAGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGGCTT 87
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AN11m TCATTAAGTCTTCTTCA 89
 AN12m TCATTAAGTCTTCTTCA 89
 AN13m TCATTAAGTCTTCTTCA 89

Figure 1

NT1p MGLHAWSEFLKDFLAGAVAAVSKTAVAPIERVKLLLOVQHASKQISAEKQ 50
 NT2p MILDAAVSFAKDFLAGGVAAALSKTAVAPIERVKLLLOVQHASKQIADKQ 50
 NT3p MIECAISFAKDFLAGGIAAALSKTAVAPIERVKLLLOVQHASKQIADKQ 50

 NT1p YKGLIDCVVRIPKEQGFLSFWRCNLANVIRYFPTQALNFAFKDKYKQIFL 100
 NT2p YKGLIDCVVRIPKEQGVLSFWRCNLANVIRYFPTQALNFAFKDKYKQIFL 100
 NT3p YKGLIDCVVRIPKEQGVLSFWRCNLANVIRYFPTQALNFAFKDKYKQIFL 100

 NT1p GGVDHFRQFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGRRA 149
 NT2p GGVDKHTQFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGRRA 149
 NT3p GGVDKHTQFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGRRA 150

 NT1p QREFEGLGDCIKKSDGIRGLYQGFNVSVQGIITYRAAYFGVYDTAKG 199
 NT2p EREFRGLGDCIKKSDGIRGLYQGFNVSVQGIITYRAAYFGVYDTAKG 199
 NT3p EREFRGLGDCIKKSDGIRGLYQGFNVSVQGIITYRAAYFGVYDTAKG 200

 NT1p MLPDPKNMHTVSWMTAQTVTAVAGLISYPFDIVRRRMMQSGRKGADIM 249
 NT2p MLPDPKNMHTVSWMTAQTVTAVAGLISYPFDIVRRRMMQSGRKGADIM 249
 NT3p MLPDPKNMHTVSWMTAQTVTAVAGLISYPFDIVRRRMMQSGRKGADIM 250

 NT1p YTGTVDCWRKIAEDEGKAFKCAWSNVLRGMGCAFVLVLYDELKKYV. 298
 NT2p YTGTVDCWRKIAEDEGKAFKCAWSNVLRGMGCAFVLVLYDELKKYT. 299
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Figure 2

104120-16011860

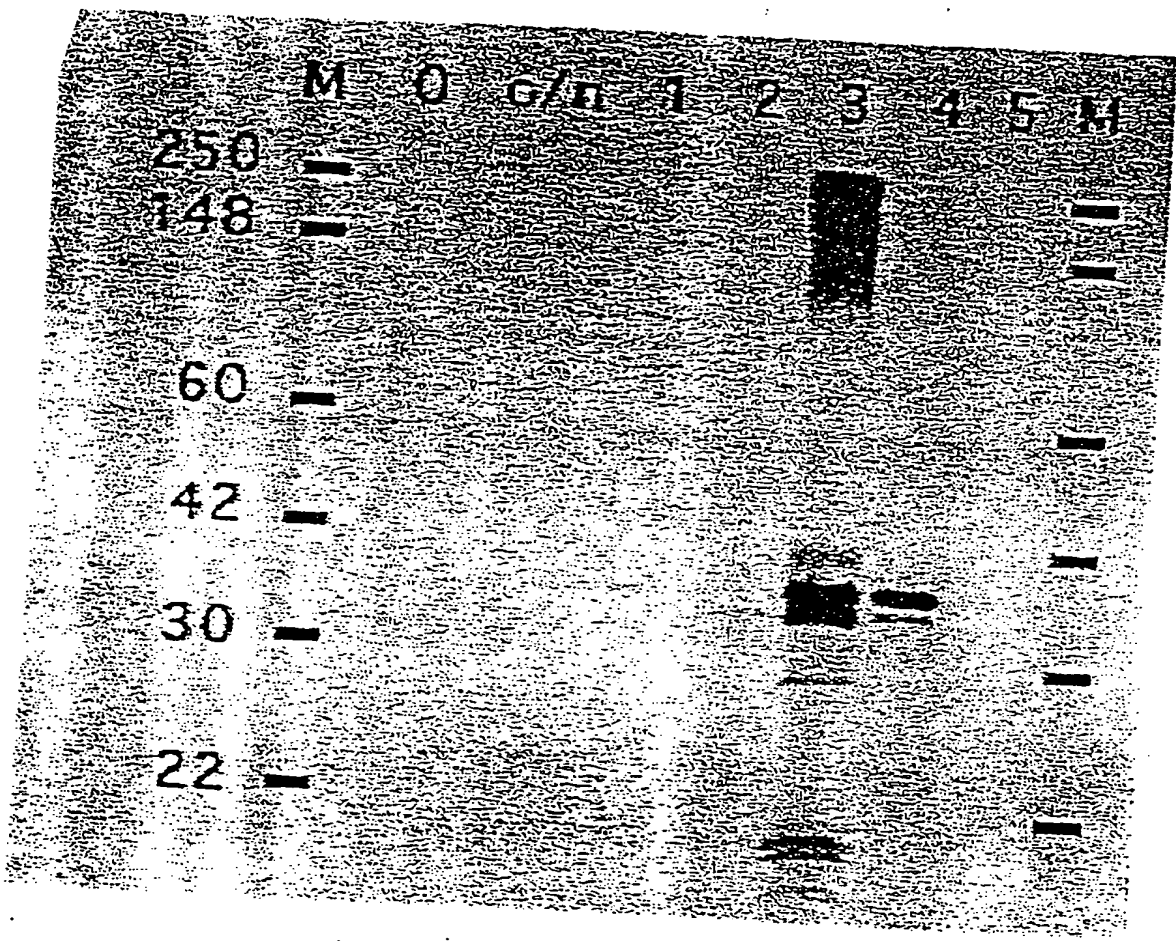


Figure 3

0981004-03440

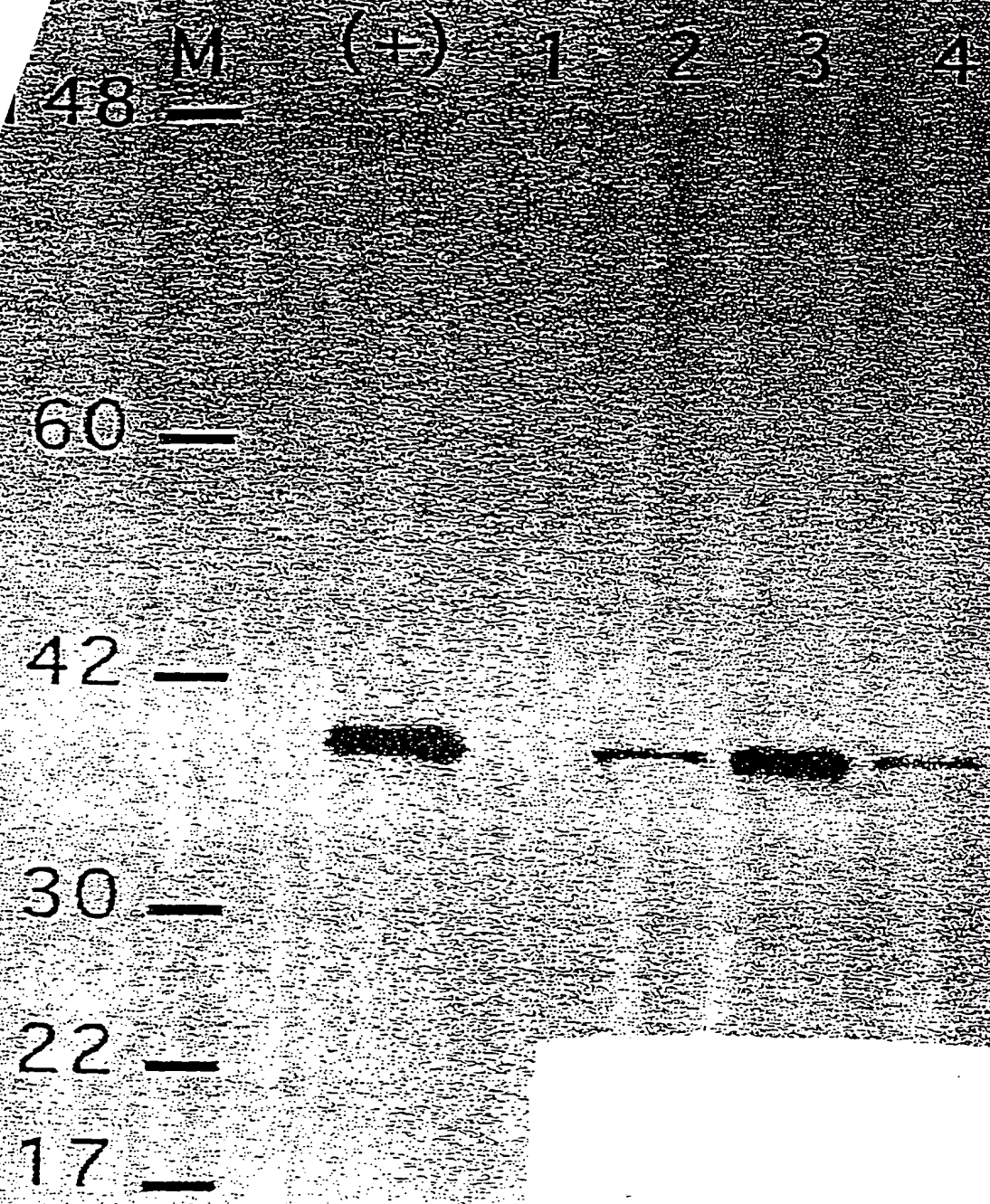


Figure 4

05811094-034401

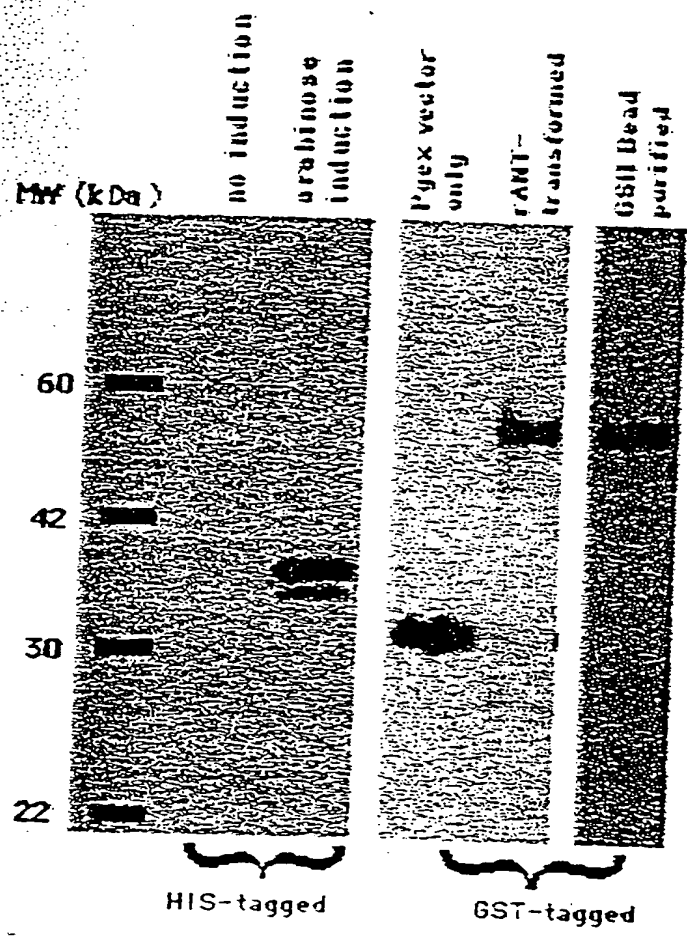


Figure 5

SDS-PAGE gel showing the purification of a 35 kDa protein. The gel has 10 lanes. Lanes 1-3 are cell lysate, lane 4 is cytosol, lane 5 is mitochondria, lane 6 is SMP, lane 7 is plasma membrane, lane 8 is Ni bead, and lanes 9-10 are purified protein. Molecular weight markers (60, 42, 30, 22 kDa) are on the left. A prominent band at approximately 35 kDa is visible in lanes 1-7 and 9-10.

Figure 6

1041120-46014860

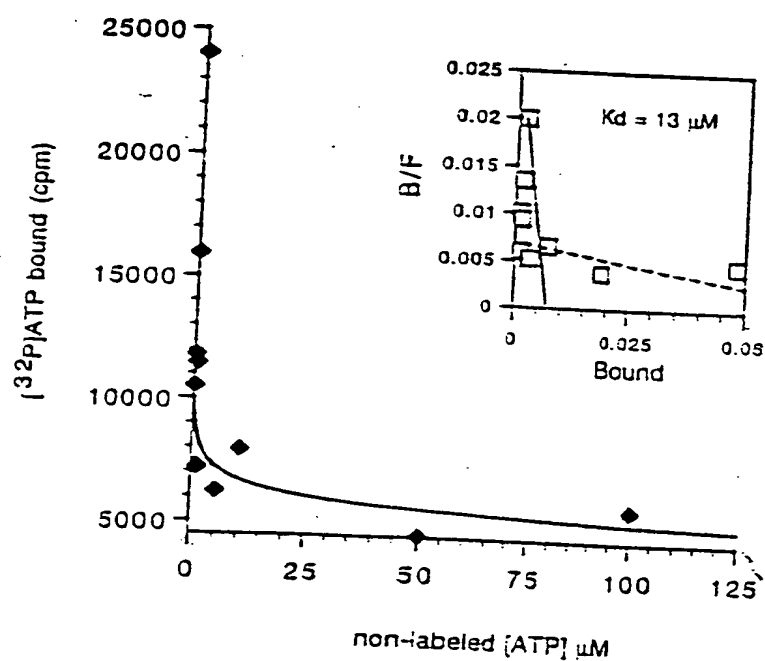


Figure 7

104100-46011860

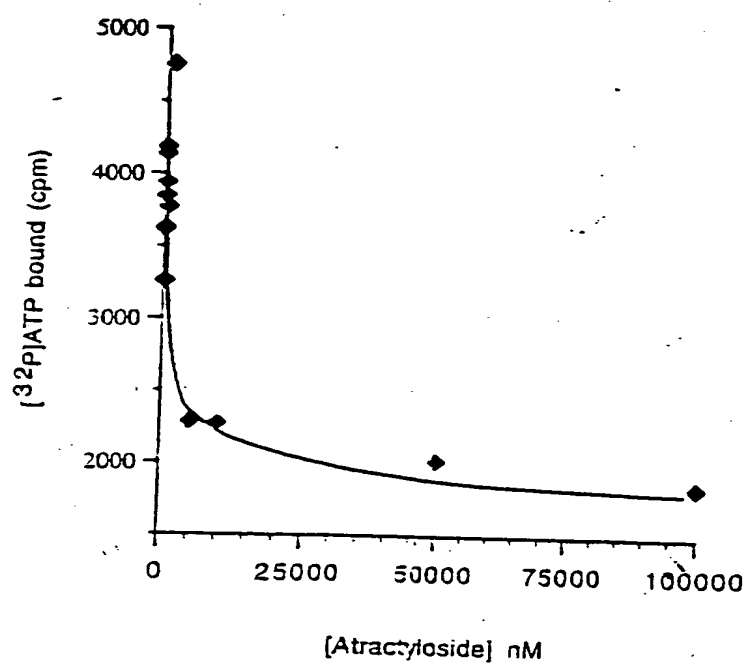


Figure 8

104720-16011860

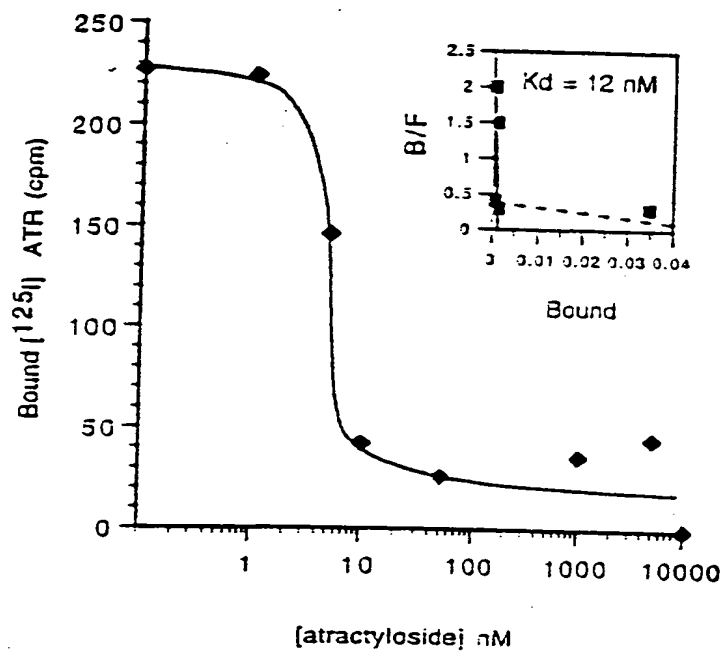


Figure 9

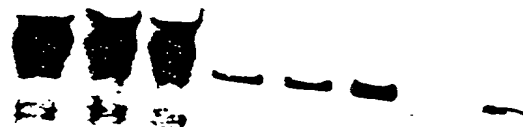


Figure 10 -

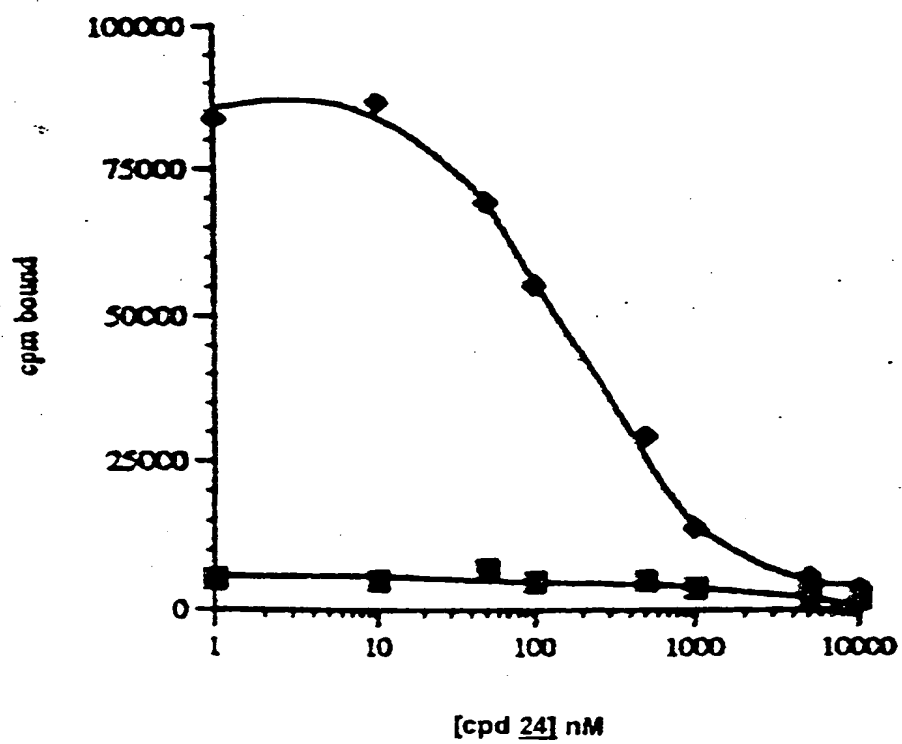


Figure 11

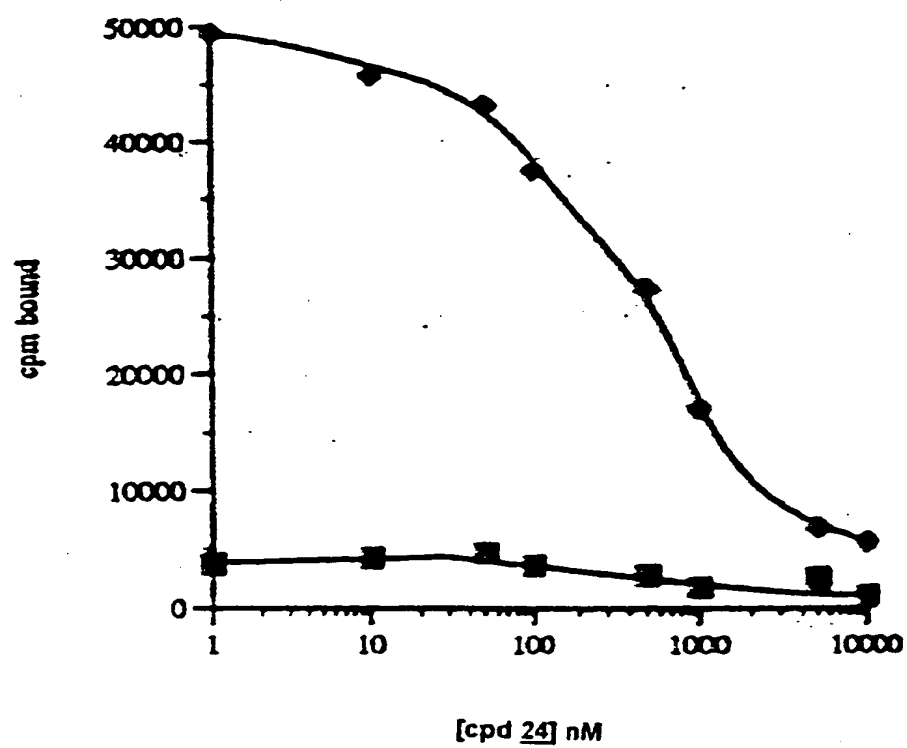


Figure 12

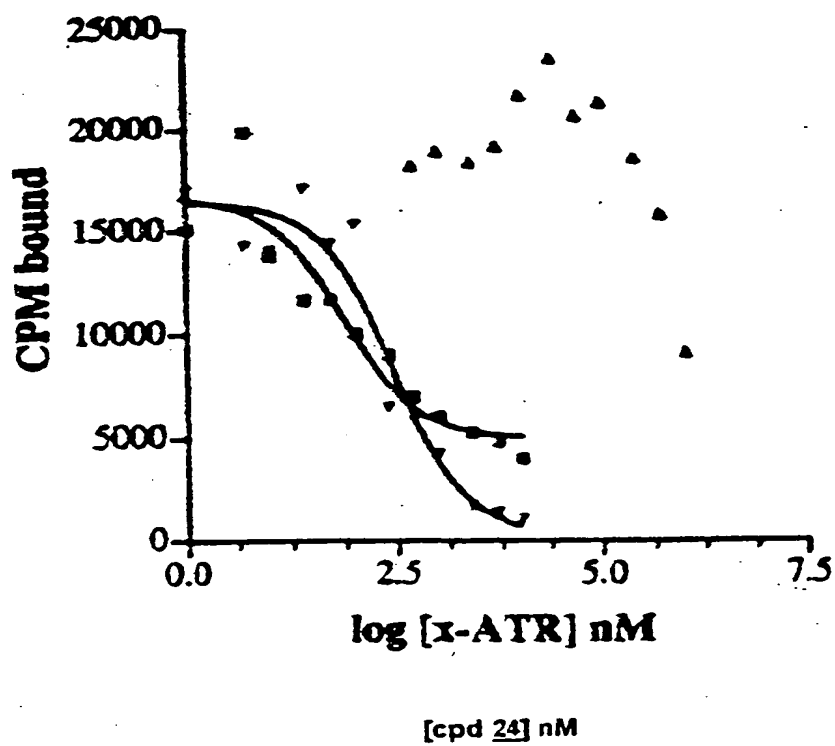


Figure 13

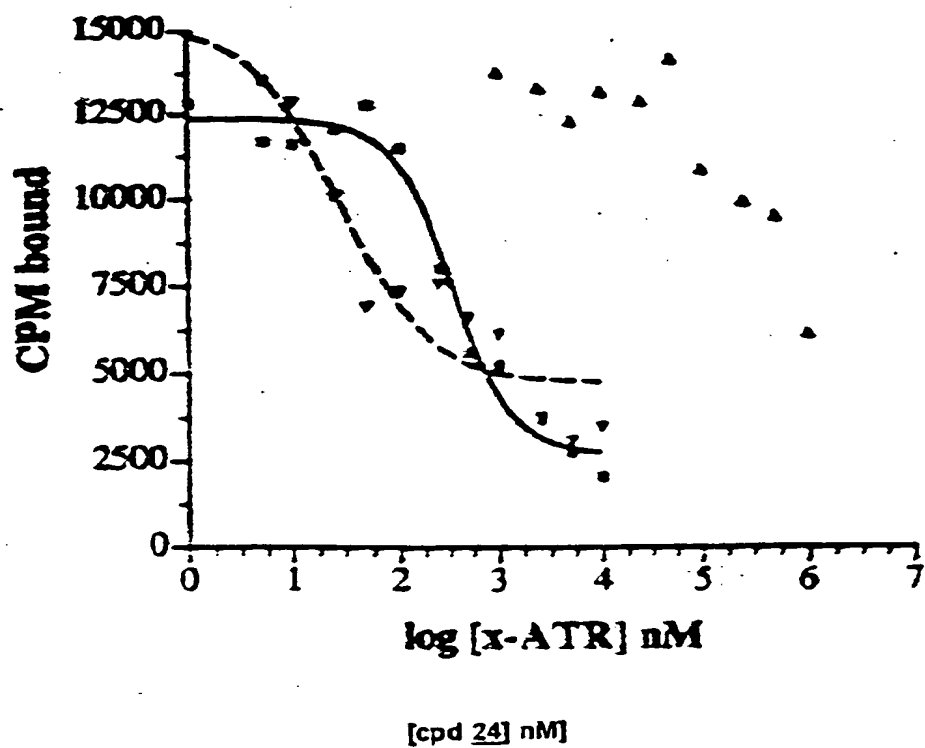


Figure 14

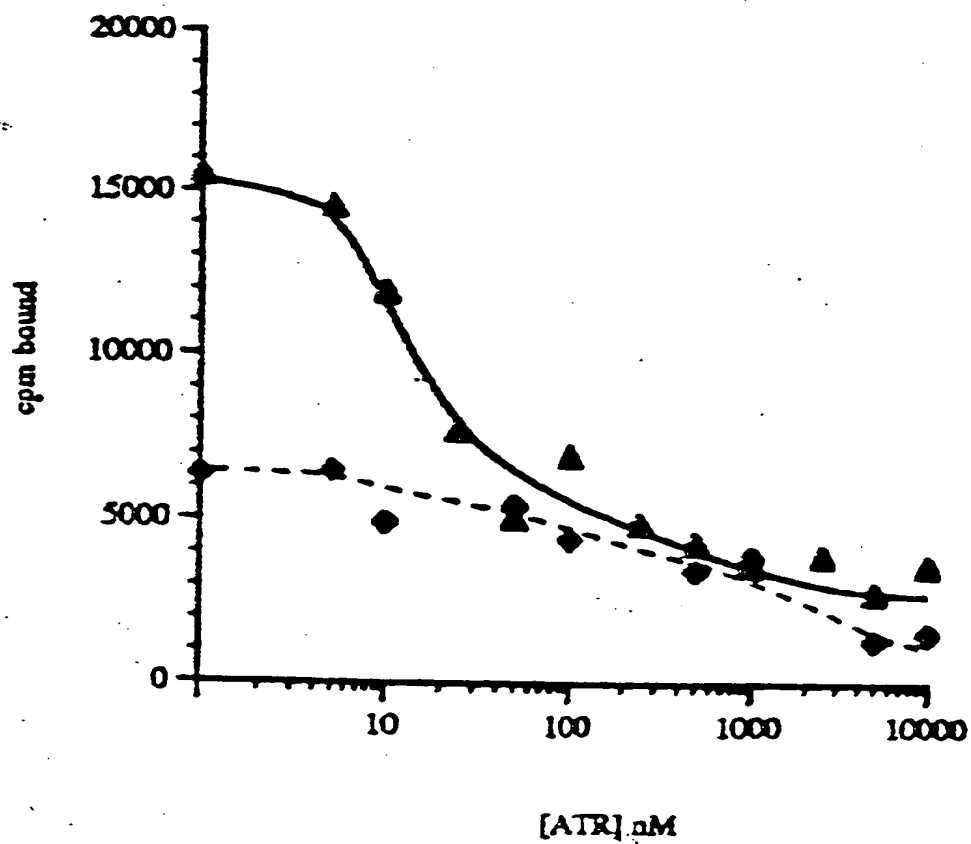


Figure 15

104120-46012360

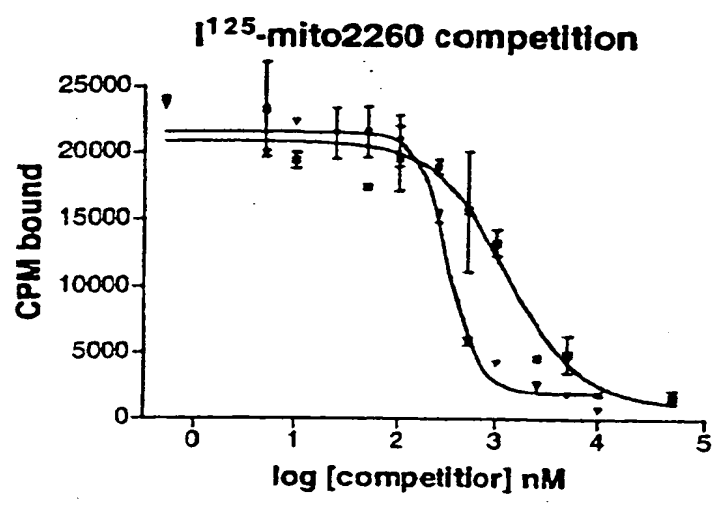


Figure 16

104160-1001250

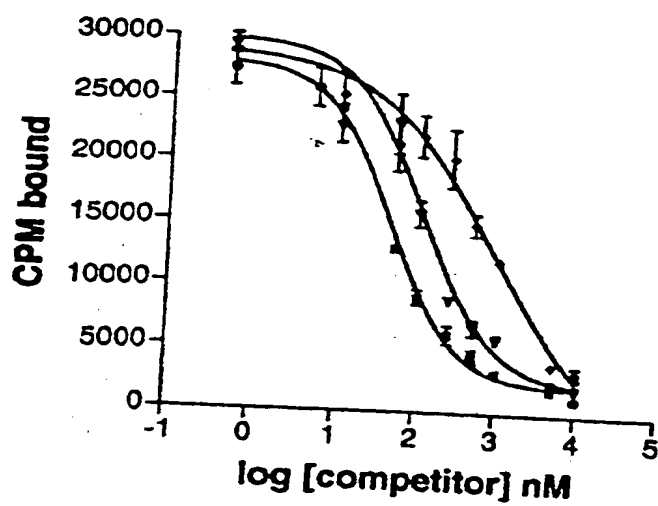


Figure 17

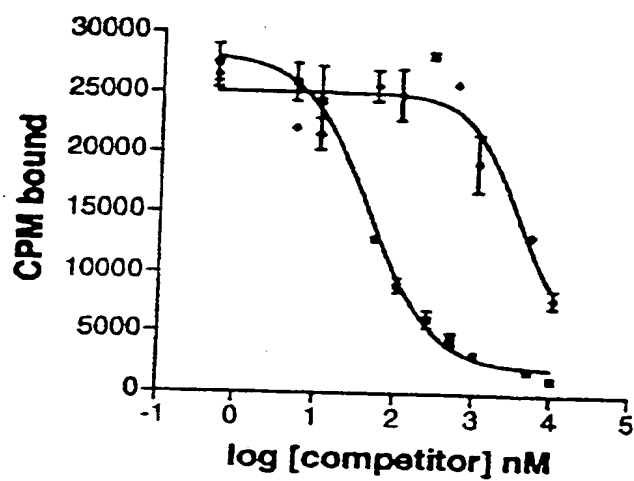


Figure 18

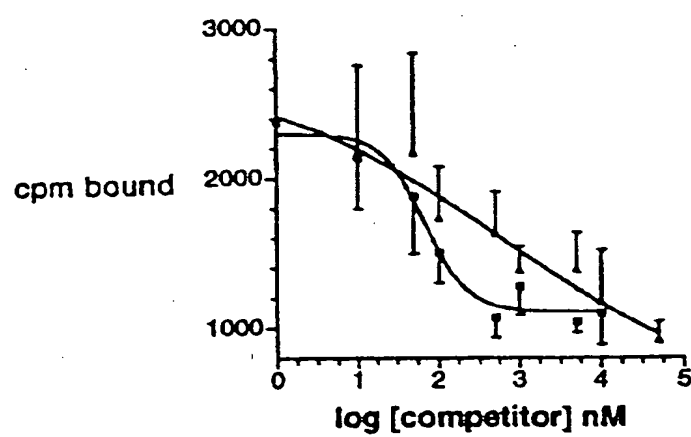


Figure 19